# Data Analysis (Prof. Ugo Ala) - R Practical N

# Cognome Nome, Cognome Nome, Cognome Nome

# 01-01-0000

# Index

ın	Introduction		
	Environment	1	
	Working directory and Packages	2	
Sl	pobina template	3	
	Header	3	
	Introduction	3	
SI	bobina template	5	
	Header	5	
	Introduction	6	
	Notes and suggestions	7	
$\mathbf{T}$	itle	8	
	Render	9	
	Warnings	O	

## Introduction

#### **Environment**

The exrcise was run in a Docker, at the moment only aversion with JupyterLab is available. The image can be pulled from GitHub:

```
docker pull ghcr.io/maiolino-au/data_analysis:latest
```

To run it open a terminal in the working directory and run this:

• In Windows

• In Linux / MacOS

Repository link: https://github.com/Maiolino-Au/Data\_Analysis

The datas used are available in the repository or on moodle.

The scripts assume that the working directory is the same where the data are stored.

### Working directory and Packages

First of all, we need to set the correct working directory: all the commands assume that the datas are stored in the working directory. I worked in a docker container to which i have shared a directory from my PC, called /sharedFolder inside the docker. In the directory there is one specific for this lesson, called Practical\_1. Therefore:

```
setwd("/sharedFolder/Practical_1/")
```

Then we need to load the packages we are going to use. I used suppressPackageStartupMessages() to avoid printing all the startup messages of each package.

```
suppressPackageStartupMessages({
    library(phyloseq)
    library(dplyr)
    library(tidyr)
    library(stringr)
    library(microbiome)
    library(microbial)
    library(vegan)
    library(usedist)
    library(ggplot2)
    library(nortest)
    library(car)
})
```

# Sbobina template

Here you find the Rmarkdown template for the sbobina and the pdf rendered from it.

#### Header

```
Here there are the settings for the file, you need to modify * Names * Date
You can modify * toc_depth: 2 if you want more, or fewer, title levels displaied in the table of content/index
title: "Data Analysis (Prof. Ugo Ala) - R Practical N"
author: "Cognome Nome, Cognome Nome, Cognome Nome"
date: "01-01-0000"
output:
 pdf_document:
    latex_engine: xelatex
    keep_tex: true
    toc: true
    toc_depth: 2
header-includes:
  - \usepackage{fvextra}
  - \usepackage{fancyhdr}
  - \DefineVerbatimEnvironment{Highlighting}{Verbatim}{breaklines,breakanywhere=true,commandchars=\\\{\
  - \fvset{breaklines=true, breakanywhere=true}
  - \renewcommand{\contentsname}{Index}
  - \AtBeginDocument{
      \pagestyle{fancy}
      \fancyhead[L]{}
      \fancyhead[R]{}
      \fancyhead[C]{Data Analysis - R Practical N - 01-01-0000 - Cognome N., Cognome N., Cognome N.}
      \fancyfoot[C]{\thepage}
      \renewcommand{\sectionmark}[1]{}
      \renewcommand{\subsectionmark}[1]{}
    }
\thispagestyle{empty}
\newpage
\pagenumbering{arabic}
\setcounter{page}{1}
```

#### Introduction

Leave this section

```
# Introduction

## Environment

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available. The image can be pulled from GitHub:
```

```
```sh
docker pull ghcr.io/maiolino-au/data_analysis:latest
To run it open a terminal in the working directory and run this:
* In Windows
```powershell
@echo off
set "CURRENT DIR=%cd%"
docker run -it --rm -p 8787:8787 -v "%CURRENT_DIR%:/sharedFolder"

→ ghcr.io/maiolino-au/data_analysis:latest

* In Linux / MacOS
```sh
docker run -it --rm -p 8787:8787 -v .:/sharedFolder

ghcr.io/maiolino-au/data_analysis:latest
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\newpage
```

For the this section \* change setwd("/sharedFolder/Practical\_1/") with the correct directory (remember that Practical\_1 is in the sharedFolder, so it is shared to the container from your computer) \* add packages if needed

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First of all, we need to set the correct working directory: all the commands assume that
the datas are stored in the working directory. I worked in a docker container to
which i have shared a directory from my PC, called '/sharedFolder' inside the docker.
In the directory there is one specific for this lesson, called 'Practical_1'.
Therefore:

""
setwd("/sharedFolder/Practical_1/")

"Then we need to load the packages we are going to use. I used
"suppressPackageStartupMessages()" to avoid printing all the startup messages of each
package.

""
r
```

```
suppressPackageStartupMessages({
    library(phyloseq)
    library(tidyr)
    library(stringr)
    library(microbiome)
    library(microbial)
    library(vegan)
    library(usedist)
    library(ggplot2)
    library(nortest)
    library(car)
})
```

# Sbobina template

#### Header

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```
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You can modify * toc_depth: 2 if you want more, or fewer, title levels displaied in the table of content/index
```

title: "Data Analysis (Prof. Ugo Ala) - R Practical N" author: "Cognome Nome, Cognome Nome, Cognome Nome" date: "01-01-0000" output: pdf\_document: latex\_engine: xelatex keep\_tex: true toc: true toc\_depth: 2 header-includes: - \usepackage{fvextra} - \usepackage{fancyhdr} - \DefineVerbatimEnvironment{Highlighting}{Verbatim}{breaklines,breakanywhere=true,commandchars=\\\{\ - \fvset{breaklines=true, breakanywhere=true} - \renewcommand{\contentsname}{Index} - \AtBeginDocument{ \pagestyle{fancy} \fancyhead[L]{} \fancyhead[R]{} \fancyhead[C]{Data Analysis - R Practical N - 01-01-0000 - Cognome N., Cognome N., Cognome N.} \fancyfoot[C]{\thepage} \renewcommand{\sectionmark}[1]{} \renewcommand{\subsectionmark}[1]{}

```
\thispagestyle{empty}
\newpage
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\setcounter{page}{1}
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#### Introduction

Leave this section

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@echo off
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···sh
docker run -it --rm -p 8787:8787 -v .:/sharedFolder

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```
## Working directory and Packages
```

```
First of all, we need to set the correct working directory: all the commands assume that
_{\mathrel{\circlearrowleft}} the datas are stored in the working directory. I worked in a docker container to
which i have shared a directory from my PC, called `/sharedFolder` inside the docker.
□ In the directory there is one specific for this lesson, called `Practical_1`.
→ Therefore:
... r
setwd("/sharedFolder/Practical_1/")
Then we need to load the packages we are going to use. I used
→ `suppressPackageStartupMessages()` to avoid printing all the startup messages of each
→ package.
suppressPackageStartupMessages({
    library(phyloseq)
    library(dplyr)
    library(tidyr)
    library(stringr)
    library(microbiome)
    library(microbial)
    library(vegan)
    library(usedist)
    library(ggplot2)
    library(nortest)
    library(car)
})
\newpage
```

### Notes and suggestions

There are up to 6 levels of titles (from # to #####), only level 1 and 2 will be shown in the table of content (Index), you can cahge it with toc\_depth

Use \newpage for ending the page

```
# Title
text text text

* lista
* lista

text text text

1. lista numerata
2. lista numerata
1. funziona anche se mettete un numero a caso (nel rendere vedete un 3)
```

```
bisogna mettere una rigavuota tra due cose
per far sì che siano
separate
importante
* per
* liste (specifico per Rmarkdown, in normal markdown you can omit the empty line right
→ before the list)
triplette di backtick per un blocco di codice, singolo backtick per una riga di codice
→ `mm <- c("m", "m")` che potete inerire nel testo. utile per dire "ho usato il comando
paste() per unire due stringhe"
... r
mm <- c("m", "m")
paste(mm[1], mm[2], sep = " - ")
## [1] "m - m"
una variabile definita in un blocco si salva nel documento e può essere richiamata in
→ blocchi successivi
paste(mm[1], mm[2], sep = " - ")
## [1] "m - m"
```

### Title

text text text

- lista
- lista

text text text

- 1. lista numerata
- 2. lista numerata
- 3. funziona anche se mettete un numero a caso (nel rendere vedete un 3)

bisogna mettere una rigavuota tra due cose per far sì che siano separate

importante \* per \* liste (specifico per Rmarkdown, in normal markdown you can omit the empty line right before the list)

triplette di backtick per un blocco di codice, singolo backtick per una riga di codice mm <- c("m", "m") che potete inerire nel testo. utile per dire "ho usato il comando paste() per unire due stringhe"

```
mm <- c("m", "m")
paste(mm[1], mm[2], sep = " - ")
## [1] "m - m"</pre>
```

una variabile definita in un blocco si salva nel documento e può essere richiamata in blocchi successivi

```
paste(mm[1], mm[2], sep = " - ")
## [1] "m - m"
```

#### Render

rmarkdown::render('/sharedFolder/Practical\_1/Data\_analysis\_R\_1.Rmd', output\_dir = '/sharedFolder/Practi

### Warnings

This gave me an error that made the render fail: it generated a warning containing some invisible characters. you can solve it with suppressMessages and suppressWarnings

```
wilcox.test(xx$observed ~ xx$Status)
boxplot(xx$observed ~ xx$Status)
```

Solved, the boxplot is still printed.

```
suppressMessages(suppressWarnings({
    wilcox.test(xx$observed ~ xx$Status)
    boxplot(xx$observed ~ xx$Status)
}))
```

A similar problem presented itself with the lines right below: bidwidth was not specified and the message with which the system notified you that the default values were used caused problems. The previous solution didn't work, so I specified the bidwidth. You could put a specific number but the resulting dot depends on the scale of the plot so the same value (this kind of plot was used 6 times) resulted in widely different dots, some covering the entire image.

```
ggplot(xx, aes(x = Status, y = observed, fill = Status)) +
    geom_boxplot() +
    geom_dotplot(
        binaxis = "y", stackdir = "center",
        binwidth = diff(range(xx$observed, na.rm = TRUE)) / 30 # sets the width of the
        dots in the dotplot, put explitly for reasons regarding Rmarkdown
)
```